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Sequence		Length	Code
VLAEAMSQV	(SEQ ID NO:70)	9	A
ILKEPVHGV	(SEQ ID NO:71)	9	B
TLNFPISPI	(SEQ ID NO:72)	9	C
SLLNATDIAV	(SEQ ID NO:73)	10	D
QMAVFIHNFK	(SEQ ID NO:74)	10	E
VTVYYGVPVWK	(SEQ ID NO:75)	11	F
FPVRPQVPL	(SEQ ID NO:76)	9	G
YPLASLRSLF	(SEQ ID NO:77)	10	H
VTYQYMDDLY	(SEQ ID NO:78)	10	I
IYQEPFKNL	(SEQ ID NO:79)	9	J
IWGCSGKLI	(SEQ ID NO:80)	9	K

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AA	C+1 ranking	N-1 ranking
K	2.20	0.64
C	2.00	1.00
N	2.00	0.00
G	1.80	1.33
T	1.50	0.00
A	1.33	1.21
F	1.33	1.00
S	1.33	0.00
W	1.20	0.00
Q	1.20	0.00
R	1.17	1.57
M	1.00	0.00
Y	1.00	0.75
I	0.86	0.50
L	0.75	2.20
V	0.00	1.19
D	0.00	0.00
H	0.00	0.00
E	0.00	0.00
P	0.00	0.00

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Motif Specification

XXXX(FY)XX(LIMV)	(SEQ ID NOS:7-14)
XXXX(FY)XXX(LIMV)	(SEQ ID NOS:15-22)
XXXXNXXX(LIMV)	(SEQ ID NOS:27-30)
XXXXNXXXX(LIMV)	(SEQ ID NOS:341-344)
X(LM)XXXXXXV	(SEQ ID NOS:31-32)
X(LM)XXXXXXXV	(SEQ ID NOS:33-34)
X(LMVT)XXXXXX(KRY)	(SEQ ID NOS:345-356)
X(LMVT)XXXXXXX(KRY)	(SEQ ID NOS:357-368)
XPXXXXXX(LIMVF)	(SEQ ID NOS:59-63)
XPXXXXXXX(LIMVF)	(SEQ ID NOS:64-68)

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FIGURE 11A

Junctional Analyzer run on Saturday, February 26, 2000 09:06:23 pm.

The following non-zero AA weights will be used.

AA	N-1 ranking	C+1 ranking
A	1.21	1.33
C	1.00	2.00
F	1.00	1.33
G	1.33	1.80
I	0.50	0.86
K	0.64	2.20
L	2.20	0.75
M	0.00	1.00
N	0.00	2.00
Q	0.00	1.20
R	1.57	1.17
S	0.00	1.33
T	0.00	1.50
V	1.19	0.00
W	0.00	1.20
Y	0.75	1.00

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The following 10 motif specifications will be used to search for junctionals.

Count	Motif Specification
1	XXXX(FY)XX(LIMV) (SEQ ID NOS:7-14)
2	XXXX(FY)XXX(LIMV) (SEQ ID NOS:15-22)
3	XXXXNXXX(LIMV) (SEQ ID NOS:27-30)
4	XXXXNXXXX(LIMV) (SEQ ID NOS:341-344)
5	X(LM)XXXXXXV (SEQ ID NOS:31-32)
6	X(LM)XXXXXXXV (SEQ ID NOS:33-34)
.7	X(LMVT)XXXXXX(KRY) (SEQ ID NOS:345-356)
8	X(LMVT)XXXXXXX(KRY)(SEQ ID NOS:357-368)
9	XPXXXXXX(LIMVF) (SEQ ID NOS:59-63)
10	XPXXXXXXX(LIMVF)(SEQ ID NOS:64-68)

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Code	Peptide		Length
A	VLAEAMSQV	(SEQ ID NO:70)	9
B	ILKEPVHGV	(SEQ ID NO:71)	9
C	TLNFPISPI	(SEQ ID NO:72)	9
D	SLLNATDIAV	(SEQ ID NO:73)	10
E	QMAVFIHNFK	(SEQ ID NO:74)	10
F	VTVYYGVPVWK	(SEQ ID NO:75)	11
G	FPVRPQVPL	(SEQ ID NO:76)	9
H	YPLASLRSLF	(SEQ ID NO:77)	10
I	VIYQYMDDLY	(SEQ ID NO:78)	10
J	IYQEPFKNL	(SEQ ID NO:79)	9
K	IWGCSGKLI	(SEQ ID NO:80)	9

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MaxInsertions = 4 (208)

FIGURE 13A

EP-HIV-1090 (SEQ ID NO:81)
MGMQVQIQSLFLLLLWVPGSRGKLVGKLNWAGAAILKEPVHGVNAACPKVSFEPIKIPIHYCAPA
KAKFVAAWTLKAAAKAFPVRPQVPLGAAKLTPLCVTLGAAAVLAEAMSQVKVYLAWVPAHKG
AAAAIFQSSMTKKTTLFCASDAKNIPYNPQSQGVVKHPVHAGPIANVTVYYGVPVWKKAAAQMA
VFIHNFKNAAAYPLASLRSLFNLTFGWCFKLNRILQQLLFINAKIQNFRVYYRKAAVTIKIGGQLKK
VPLQLPPLKAMTNNPPIPV

ATGGGAATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGATCCAGA
GGAAAGCTGGTGGGCAAACTCAACTGGGCCGGAGCTGCAATCCTGAAGGAGCCCGTCCACGG
GGTGAATGCCGCTTGCCCTAAAGTCAGCTTCGAACCAATTAAGATCCCCATTCATTACTGTGC
ACCTGCCAAAGCTAAGTTTGTGGCCGCTTGGACCCTCAAGGCCGCTGCAAAAGCCTTCCAGT
GAGGCCCCAGGTGCCTCTGGGCGCCGCTAAACTCACACCACTGTGCGTCACTCTGGGAGCCGC
TGCAGTGCTGGCAGAGGCCATGTCCCAAGTGAAGGTGTATCTGGCTTGGGTGCCCGCCCACAA
GGGGGCCGCTGCAGCCATCTTTCAGTCTAGCATGACCAAGAAAACAACTCTGTTCTGTGCCTC
CGACGCTAAGAACATCCCTTATAATCCACAGTCTCAGGGCGTGGTCAAGCATCCCGTGCACGC
CGGACCTATTGCTAACGTGACCGTGTACTATGGGGTCCCAGTGTGGAAGAAAGCCGCTGCACA
GATGGCCGTGTTTATTCACAATTTCAAAAACGCCGCTGCATACCCCCTCGCCAGCCTGAGATC
CCTCTTCAACCTGACATTCGGCTGGTGCTTTAAGCTGAACCGGATCCTGCAGCAACTGCTCTTT
ATCAATGCTAAAATCCAGAACTTCCGCGTCTACTATAGGAAGGCTGCAGTGACTATCAAAATT
GGCGGACAACTGAAGAAAGTGCCTCTCCAGCTGCCCCCTCTCAAGGCAATGACCAACAATCC
CCCTATCCCAGTCTGA (SEQ ID NO:82)

HIV-CPT (SEQ ID NO:83)
MGMQVQIQSLFLLLLWVPGSRGIPIHYCAPAKAAKIQNFRVYYRKAAVTIKIGGQLKKAKFVAAW
TLKAAAKVPLQLPPLKAIFQSSMTKKLTPLCVTLGAQMAVFIHNFKGAKVYLAWVPAHKNAIPYN
PQSQGVVKAILKEPVHGVGAAALTFGWCFKLNAVLAEAMSQVNRILQQLLFINAAACPKVSFEPI
KVTVYYGVPVWKKAAHPVHAGPIANAAAYPLASLRSLFNAAATTLFCASDAKNKLVGKLNWAN
AAAFPVRPQVPLNMTNNPPIPV

ATGGGGATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGATCCAGA
GGAATCCCCATTCACTACTGCGCCCCTGCTAAGGCAGCCAAAATCCAGAACTTCAGGGTGTAT
TACAGAAAGGCTGCAGTCACCATTAAAATCGGCGGACAACTGAAGAAAGCCAAGTTTGTGGC
CGCTTGGACACTCAAGGCCGCTGCAAAGGTCCCACTGCAGCTCCCCCCTCTGAAGGCCATCTT
CCAGAGCTCCATGACTAAGAAACTGACCCCACTGTGTGTGACACTCGGGGCCCAGATGGCTGT
GTTCATCCATAATTTTAAAGGCGCCAAGGTCTACCTGGCTTGGGTGCCCGCACACAAGAACGC
CATTCCTTACAATCCACAGTCTCAAGGAGTGGTCAAAGCTATTCTGAAGGAGCCCGTGCACGG
GGTGGGCGCCGCTGCACTCACTTTCGGATGGTGCTTTAAACTGAACGCCGTGCTGGCTGAAGC
CATGAGCCAGGTCAATCGGATCCTGCAGCAACTGCTCTTCATTAACGCCGCTGCATGTCCTAA
GGTGTCCTTCGAGCCAATCAAAGTGACCGTGTATTACGGGGTCCCCGTGTGGAAGAAAGCCGC
TCATCCTGTCCACGCAGGCCCAATCGCCAACGCCGCTGCATATCCCCTCGCCTCTCTGCGCAG
CCTGTTTAACGCCGCTGCAACAACCCTCTTTTGCGCCTCCGACGCTAAGAATAAACTGGTGGG
AAAGCTGAACTGGGCCAACGCAGCTGCATTCCCTGTGAGGCCACAGGTCCCCCTCAATATGAC
TAACAATCCCCCTATCCCAGTGTGA (SEQ ID NO:84)

FIGURE 18A

HIV-FT (SEQ ID NO:85)

MQVQIQSLFLLLLWVPGSRGKLVGKLNWAMASDFNLPPVAIFQSSMTKVTIKIGGQLKRILQQLLF
IMAVFIHNFKIPYNPQSQGVVTTLFCASDAKILKEPVHGVQMAVFIHNFKGAAVFIHNFKRCPKVSF
EPIKIQNFRVYYRLTFGWCFKLQVPLRPMTYKMTNNPPIPVTVYYGVPVWKVLAEAMSQVIPIHY
CAPAKLTPLCVTL

ATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGATCCAGAGGAAAG
CTGGTGGGGAAGCTGAACTGGGCCATGGCCAGCGATTTCAACCTGCCCCCCGTGGCCATCTTC
CAGAGCAGCATGACCAAGGTGACCATCAAGATCGGGGGGCAGCTGAAGAGGATCCTGCAGCA
GCTGCTGTTCATCATGGCCGTGTTCATCCACAACTTCAAGATCCCCTACAACCCCCAGAGCCA
GGGGGTGGTGACCACCCTGTTCTGCGCCAGCGATGCCAAGATCCTGAAGGAGCCCGTGCACG
GGGTGCAGATGGCCGTGTTCATCCACAACTTCAAGGGCGCCGCCGTGTTCATCCACAACTTCA
AGAGGTGCCCCAAGGTGAGCTTCGAGCCCATCAAGATCCAGAACTTCAGGGTGTACTACAGG
CTGACCTTCGGGTGGTGCTTCAAGCTGCAGGTGCCCCTGAGGCCCATGACCTACAAGATGACC
AACAACCCCCCCATCCCCGTGACCGTGTACTACGGGGTGCCCGTGTGGAAGGTGCTGGCCGAG
GCCATGAGCCAGGTGATCCCCATCCACTACTGCGCCCCCGCCAAGCTGACCCCCCTGTGCGTG
ACCCTG (SEQ ID NO:86)

FIGURE 18B

HIV-TC (SEQ ID NO:87)
MGMQVQIQSLFLLLLWVPGSRGYWQATWIPEWKAIFQSSMTKKVYLAWVPAHKNAACPKVSFE
PIKHPVHAGPIANLTFGWCFKLNKMIGGIGGFIKFRDYVDRFYKAAARILQQLLFINTTLFCASDAK
NQMVHQAISPRGAKLVGKLNWAGAAAIYETYGDTWKAAQVPLRPMTYKGAAAVTVLDVGDAY
NAAARYLKDQQLLNTLNFPISPINMTNNPPIPVNAPYNTPVFAIKAAAVPLQLPPLKAAIPYNPQSQ
GVVKALLQLTVWGIGAAILKEPVHGVNAAAFPISPIETVKVWKEATTTLFKAAAVTIKIGGQLKKI
YQEPFKNLKAAAVLAEAMSQVNLVGPTPVNIGAAAEVNIVTDSQYKAAAIPIHYCAPAKAVIYQY
MDDLYKAAAQMAVFIHNFKNAATYQIYQEPFKPYNEWTLELKAKIQNFRVYYRKAFPVRPQVPL
GAAAIWGCSGKLIKVMIVWQVDRNAAKAACWWAGIKAKFVAAWTLKAAAKLTPLCVTLNAAM
ASDFNLPPVKSLLNATDIAVNVTVYYGVPVWKKAAAAIIRILQQLKRAMASDFNLNAAAYPLASL
RSLF

ATGGGGATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGATCTAGA
GGATACTGGCAAGCTACTTGGATTCCAGAATGGAAAGCTATCTTTCAATCCTCAATGACGAAG
AAGGTATACCTGGCATGGGTCCCAGCACACAAGAACGCCGCTTGCCCAAAGGTGTCCTTTGAA
CCCATTAAACACCCAGTGCACGCAGGGCCAATAGCGAATTTGACATTCGGGTGGTGCTTCAAA
CTAAACAAAATGATCGGCGGCATTGGAGGCTTTATCAAGTTTAGAGATTACGTGGACCGATTC
TATAAAGCCGCTGCCCGTATACTCCAGCAGCTACTATTCATCAACACCACTCTCTTCTGCGCTT
CAGACGCTAAGAACCAAATGGTACACCAAGCCATAAGCCCTAGAGGAGCCAAGCTCGTAGGG
AAATTAAATTGGGCGGGTGCAGCAGCAATCTACGAGACTTACGGCGATACCTGGAAAGCAGC
CCAGGTTCCGTTACGCCCAATGACCTATAAAGGCGCAGCAGCAGTAACAGTTCTAGATGTAGG
AGACGCTTACAACGCTGCCGCAAGATACCTAAAAGATCAGCAGTTACTCAACACACTAAATTT
CCCAATTAGCCCGATAAACATGACAAATAACCCACCAATTCCCGTCAATGCTCCCTACAACAC
TCCAGTATTCGCAATCAAAGCCGCTGCTGTCCCCCTGCAGCTCCCTCCTCTGAAAGCTGCGAT
ACCTTACAACCCACAGAGCCAAGGTGTTGTCAAAGCACTGCTTCAGCTAACAGTTTGGGGAAT
TGGTGCTGCAATTCTAAAAGAGCCAGTTCATGGGGTTAACGCCGCCGCCTTCCCAATCAGTCC
TATTGAGACTGTGAAAGTATGGAAAGAAGCCACAACCACACTTTTTAAGGCAGCCGCAGTTA
CAATTAAAATAGGGGGCCAACTTAAGAAAATATACCAGGAACCTTTCAAGAATCTCAAAGCC
GCTGCAGTGCTCGCCGAGGCTATGTCACAGGTGAATTTGGTCGGACCAACACCCGTAAACATC
GGAGCCGCAGCCGAAGTGAACATAGTCACCGACTCACAGTACAAAGCCGCTGCAATACCCAT
ACATTATTGTGCTCCCGCAAAGGCCGTGATCTATCAATATATGGACGACCTGTATAAGGCCGC
CGCGCAGATGGCAGTCTTTATCCACAACTTTAAAAACGCAGCTACTTATCAGATCTACCAGGA
ACCATTCAAACCGTACAATGAGTGGACCTTGGAACTAAAGGCCAAAATTCAGAACTTCAGGG
TATATTATAGAAAGCATTTCCAGTGAGGCCCCAGGTGCCTCTGGGTGCCGCAGCAATATGGG
GATGTTCTGGAAAACTGATCAAGGTGATGATTGTATGGCAAGTGGACAGAAATGCAGCTAAG
GCAGCCTGTTGGTGGGCAGGTATAAAAGCAAAGTTCGTGGCAGCATGGACGCTTAAAGCAGC
CGCAAAACTCACTCCTCTCTGCGTGACACTTAATGCAGCCATGGCCTCTGATTTCAACCTTCCC
CCTGTAAAATCCCTGCTTAATGCGACAGATATCGCAGTCAACGTAACAGTATATTATGGCGTG
CCAGTCTGGAAAAAAGCCGCCGCGGCCATAATTCGGATACTGCAGCAGCTGAAAAGAGCTAT
GGCGAGTGACTTCAACCTGAATGCGGCCGCCTACCCCTTGGCATCGTTAAGGTCACTATTTTG
A (SEQ ID NO:88)

FIGURE 18C

HCV.1 (SEQ ID NO:89)
MGMQVQIQSLFLLLLWVPGSRGLLFNILGGWVDLMGYIPLVYLVAYQATVILAGYGAGVRLIVFP
DLGVHMWNFISGIYLLPRRGPRLYLVTRHADVVLVGGVLAALLFLLLADAFLLLADARVWMNRL
IAFACTCGSSDLYLSAFSLHSYGVAGALVAFKLPGCSFSIFKTSERSQPRLIFCHSKKKFWAKHMW
NFIPFYGKAIRMYVGGVEHRQLFTFSPRRRLGVRATRKVGIYLLPNRAKFVAAWTLKAAA*

GAATTCGCCGCCACCATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGATCCAGAGGACTGC
TGTTCAACATCCTGGGGGGGTGGGTGGATCTGATGGGGTACATCCCCCTGGTGTACCTGGTGGCCTACCAGGCCACCGT
GATCCTGGCCGGGTACGGGGCCGGGGTGAGGCTGATCGTGTTCCCCGATCTGGGGGTGCACATGTGGAACTTCATCAGC
GGGATCTACCTGCTGCCCAGGAGAGGACCTAGACTGTACCTGGTGACTAGACACGCTGATGTGGTGCTGGTGGGAGGAG
TGCTGGCTGCTCTGCTGTTTCTGCTGCTGGCTGATGCTTTCCTGCTGCTGGCTGATGCTAGAGTGTGGATGAACAGACT
GATCGCTTTCGCTTGTACATGTGGAAGCTCCGATCTGTATCTGAGCGCTTTCAGCCTGCACAGCTACGAGTGGCTGGA
GCTCTGGTGGCTTTTAAGCTGCCTGGATGTAGCTTTAGCATCTTTAAGACCAGCGAAAGAAGCCAGCCTAGACTGATCT
TTTGTCACAGCAAGAAGAAGTTTTGGGCTAAGCACATGTGGAATTTTATCCCTTTCTATGGAAAGGCTATCAGAATGTA .
TGTGGGAGGAGTGGAACACAGACAGCTGTTTACATTTAGCCCTAGAAGGAGACTGGGAGTGAGAGCTACAAGAAAGGTG
GGAATCTATCTGCTGCCTAATAGATGAAAGCTTGGG* (SEQ ID NO:90)

HCV.2 (SEQ ID NO:91)
MGMQVQIQSLFLLLLWVPGSRGDLMGYIPLVAKFVAAWTLKAAALLFLLLADALIFCHSKKKQLF
TFSPRRYLVTRHADVYLLPRRGPRLCTCGSSDLYHMWNFISGIFWAKHMWNFAKFVAAWTLKAA
AILAGYGAGVYLVAYQATVGVAGALVAFKIPFYGKAIRMYVGGVEHRVLVGGVLAAFLLLADA
RVLPGCSFSIFAKFVAAWTLKAAAKTSERSQPRRLGVRATRKRLIVFPDLGVWMNRLIAFALSAFS
LHSYLLFNILGGWVVGIYLLPNR*

GAATTCGCCGCCACCATGGGAATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGG
GTGCCCGGATCCAGAGGAGATCTGATGGGATATATCCCTCTGGTGGCTAAGTTTGTGGCTGCT
TGGACACTGAAGGCTGCTGCTCTGCTGTTTCTGCTGCTGGCTGATGCTCTGATCTTCTGTCACA
GCAAGAAGAAGCAGCTGTTTACATTTAGCCCAAGAAGATATCTGGTGACAAGACACGCTGAT
GTGTATCTGCTGCCTAGACGCGGACCTAGACTGTGTACATGTGGAAGCTCCGATCTGTATCAC
ATGTGGAACTTTATCAGCGGAATCTTTTGGGCTAAGCACATGTGGAATTTCATCCTGGCTGGA
TATGGAGCTGGAGTGTATCTGGTGGCTTATCAGGCTACAGTGGGAGTGGCTGGAGCTCTGGTG
GCTTTCAAGATCCCATTCTATGGAAAGGCTATCAGAATGTATGTGGGAGGAGTGGAACACAG
AGTGCTGGTGGGAGGAGTGCTGGCTGCTTTCCTGCTGCTGGCTGATGCTAGAGTGCTGCCAGG
ATGTAGCTTTAGCATCTTCAAGACTTCCGAACGCTCCCAGCCTAGAAGACTGGGAGTGAGAGC
TACAAGGAAGAGACTGATCGTGTTTCCAGATCTGGGAGTGTGGATGAATAGACTGATCGCTTT
CGCTCTGAGCGCTTTCAGCCTGCACAGCTATCTGCTGTTCAACATCCTGGGAGGATGGGTGGT
GGGAATCTATCTGCTGCCAAACAGATGAAAGCTT (SEQ ID NO:92)

HCV.3s1 (SEQ ID NO:93)
MGMQVQIQSLFLLLLWVPGSRGYLVAYQATVAKFVAAWTLKAAALLFLLLADALIFCHSKKKYL
VTRHADVLGFGAYMSKCTCGSSDLYHMWNFISGIFWAKHMWNF*

GAATTCGCCGCCACCATGGGAATGCAGGTGCAGATCCAAAGCCTGTTTCTGCTCCTCCTGTGG
GTGCCCGGATCCAGAGGATACCTCGTCGCCTACCAGGCCACTGTGGCTAAATTCGTGGCAGCC
TGGACACTGAAAGCTGCAGCTCTGCTCTTCCTGCTCCTGGCCGATGCACTCATCTTCTGCCATT
CCAAGAAAAAGTATCTGGTCACCAGACATGCTGACGTGCTGGGGTTTGGCGCCTACATGAGC
AAGTGCACCTGTGGCAGCTCCGACCTGTATCACATGTGGAACTTTATTTCTGGAATCTTTTGGG
CCAAGCACATGTGGAATTTCTGAAAGCTT (SEQ ID NO:94)

FIGURE 18D

HCV.3s2 (SEQ ID NO:95)
MGMQVQIQSLFLLLLWVPGSRGVLVGGVLAAAKFVAAWTLKAAAFLLLADARVLSAFSLHSYIL
AGYGAGVWMNRLIAFAIPFYGKAIVAGALVAFKVGIYLLPNR*

GAATTCGCCGCCACCATGGGAATGCAGGTGCAGATCCAAAGCCTGTTTCTGCTCCTCCTGTGG
GTGCCCGGATCCAGAGGAGTCCTGGTGGGCGGCGTCCTGGCCGCTGCTAAGTTTGTCGCTGCT
TGGACACTGAAGGCAGCCGCTTTCCTGCTCCTGGCAGACGCCAGGGTGCTGTCTGCCTTCAGC
CTCCACTCCTACATCCTCGCAGGGTATGGCGCAGGCGTGTGGATGAATCGGCTGATCGCCTTT
GCCATTCCATTCTATGGGAAAGCCATTGTGGCTGGCGCCCTGGTGGCATTCAAGGTCGGGATC
TACCTCCTGCCTAACCGCTGAAAGCTT (SEQ ID NO:96)

HCV.3s2(-3) (SEQ ID NO:97)
MGMQVQIQSLFLLLLWVPGSRGVLVGGVLAAAKFVAAWTLKAAAFLLLADARVLSAFSLHSYIL
AGYGAGVWMNRLIAFA*

GAATTCGCCGCCACCATGGGAATGCAGGTGCAGATCCAAAGCCTGTTTCTGCTCCTCCTGTGG
GTGCCCGGATCCAGAGGAGTCCTGGTGGGCGGCGTCCTGGCCGCTGCTAAGTTTGTCGCTGCT
TGGACACTGAAGGCAGCCGCTTTCCTGCTCCTGGCAGACGCCAGGGTGCTGTCTGCCTTCAGC
CTCCACTCCTACATCCTCGCAGGGTATGGCGCAGGCGTGTGGATGAATCGGCTGATCGCCTTT
GCCTGAGGATCC (SEQ ID NO:98)

HCV.3s3 (SEQ ID NO:99)
MGMQVQIQSLFLLLLWVPGSRGDLMGYIPLVAKFVAAWTLKAAARLGVRATRKLLFNILGGWV
RMYVGGVEHRRLIVFPDLGVGVAGALVAFKLPGCSFSIFKTSERSQPRQLFTFSPRRYLLPRRGPRL

GAATTCGCCGCCACCATGGGAATGCAGGTGCAGATCCAAAGCCTGTTTCTGCTCCTCCTGTGG
GTGCCCGGATCCAGAGGAGACCTGATGGGCTACATCCCTCTCGTGGCCAAGTTTGTGGCAGCT
TGGACCCTGAAGGCCGCTGCCAGACTGGGAGTGCGCGCTACACGGAAACTCCTGTTTAACATC
CTGGGAGGGTGGGTGCGGATGTACGTCGGAGGCGTCGAGCACAGAAGGCTCATTGTCTTTCC
AGATCTCGGCGTGGGCGTCGCAGGCGCACTCGTGGCCTTCAAACTGCCAGGGTGCAGCTTCAG
CATTTTCAAGACCTCCGAACGCTCCCAACCCAGACAGCTGTTCACTTTCTCTCCTCGGAGGTAT
CTGCTGCCCAGACGCGGACCCAGGCTGTGAAAGCTT (SEQ ID NO:100)

HCV.PC3 (SEQ ID NO:101)
MGMQVQIQSLFLLLLWVPGSRGLLFNILGGWVKAKFVAAWTLKAAALADGGCSGGAYRLIVFPD
LGVKFWAKHMWNFIGVAGALVAFKKQLFTFSPRR*

GAATTCGCCGCCACCATGGGAATGCAGGTGCAGATCCAAAGCCTGTTTCTGCTCCTCCTGTGG
GTGCCCGGATCCAGAGGACTGCTCTTCAACATCCTGGGCGGATGGGTGAAGGCCAAGTTCGTG
GCTGCCTGGACCCTGAAGGCTGCCGCTCTGGCCGACGGGGGATGCAGCGGCGGAGCTTACAG
GCTCATTGTCTTTCCCGATCTCGGAGTCAAATTTTGGGCAAAGCACATGTGGAATTTCATCGG
GGTGGCCGGAGCCCTGGTCGCTTTTAAAAAGCAGCTCTTCACCTTCTCCCCAAGACGGTGAGG
TACC (SEQ ID NO:102)

FIGURE 18E

HCV.PC4 (SEQ ID NO:103)
MGMQVQIQSLFLLLLWVPGSRGRLGVRATRKKAKFVAAWTLKAAAKTSERSQPRNLPGCSFSIFN
DLMGYIPLVKYLLPRRGPRLNTLCGFADLMGYRMYVGGVEHR*

GAATTCGCCGCCACCATGGGAATGCAGGTGCAGATCCAAAGCCTGTTTCTGCTCCTCCTGTGG
GTGCCCGGATCCAGAGGAAGGCTGGGCGTGAGAGCCACCCGGAAGAAGGCCAAGTTCGTGGC
TGCCTGGACCCTGAAGGCTGCCGCTAAAACAAGCGAGCGCTCCCAGCCCAGGAACCTGCCTG
GATGCTCTTTCAGCATCTTTAATGACCTCATGGGGTACATTCCACTGGTGAAGTATCTGCTCCC
CAGACGGGGCCCTCGCCTGAACACTCTCTGTGGATTTGCTGATCTGATGGGGTACAGGATGTA
TGTCGGCGGAGTCGAACACAGATGAGGTACC (SEQ ID NO:104)

HCV.2431(1P) (SEQ ID NO:105)
MGMQVQIQSLFLLLLWVPGSRGVLVGGVLAAAFLLLADARVLSAFSLHSYILAGYGAGVWMNRL
IAFAGAAARLGVRATRKKAAAKTSERSQPRNLPGCSFSIFNDLMGYIPLVKYLLPRRGPRLNTLCG
FADLMGYRMYVGGVEHRKLLFNILGGWVKAAALADGGCSGGAYRLIVFPDLGVKFWAKHMWN
FIGVAGALVAFKKQLFTFSPRRNGYLVAYQATVAAALLFLLLADALIFCHSKKKYLVTRHADVLG
FGAYMSKCTCGSSDLYHMWNFISGIFWAKHMWNFKAAAAKFVAAWTLKAAA

GAATTCGCCGCCACCATGGGAATGCAGGTGCAGATCCAAAGCCTGTTTCTGCTCCTCCTGTGG
GTGCCCGGCTCCAGAGGAGTCCTGGTGGGCGGCGTCCTGGCAGCCGCTTTCCTGCTCCTGGCA
GACGCCAGGGTGCTGTCTGCCTTCAGCCTCCACTCCTACATCCTCGCAGGGTATGGCGCAGGC
GTGTGGATGAATCGGCTGATCGCCTTTGCCGGCGCTGCCGCAAGGCTGGGCGTGAGAGCCACC
CGGAAGAAGGCTGCCGCTAAAACAAGCGAGCGCTCCCAGCCCAGGAACCTGCCTGGATGCTC
TTTCAGCATCTTTAATGACCTCATGGGGTACATTCCACTGGTGAAGTATCTGCTCCCCAGACGG
GGCCCTCGCCTGAACACTCTCTGTGGATTTGCTGATCTGATGGGGTACAGGATGTATGTCGGC
GGAGTCGAACACAGAAAACTGCTCTTCAACATCCTGGGCGGATGGGTGAAGGCTGCCGCTCT
GGCCGACGGGGGATGCAGCGGCGGAGCTTACAGGCTCATTGTCTTTCCCGATCTCGGAGTCAA
ATTTTGGGCAAAGCACATGTGGAATTTCATCGGGGTGGCCGGAGCCCTGGTCGCTTTTAAAAA
GCAGCTCTTCACCTTCTCCCCAAGACGGAACGGATACCTCGTCGCCTACCAGGCCACTGTGGC
TGCAGCTCTGCTCTTCCTGCTCCTGGCCGATGCACTCATCTTCTGCCATTCCAAGAAAAAGTAT
CTGGTCACCAGACATGCTGACGTGCTGGGGTTTGGCGCCTACATGAGCAAGTGCACCTGTGGC
AGCTCCGACCTGTATCACATGTGGAACTTTATTTCTGGAATCTTTTGGGCCAAGCACATGTGG
AATTTTAAGGCCGCAGCAGCTAAATTCGTGGCAGCCTGGACACTGAAAGCAGCTGCATGAGG
ATCC (SEQ ID NO:106)

FIGURE 18F

HCV.4312(1P) (SEQ ID NO:107)
MGMQVQIQSLFLLLLWVPGSRGRLGVRATRKKAAAKTSERSQPRNLPGCSFSIFNDLMGYIPLVK
YLLPRRGPRLNTLCGFADLMGYRMYVGGVEHRKLLFNILGGWVKAAALADGGCSGGAYRLIVFP
DLGVKFWAKHMWNFIGVAGALVAFKKQLFTFSPRRNGYLVAYQATVAAALLFLLLADALIFCHS
KKKYLVTRHADVLGFGAYMSKCTCGSSDLYHMWNFISGIFWAKHMWNFKKAAAVLVGGVLAA
AFLLLADARVLSAFSLHSYILAGYGAGVWMNRLIAFANAAAKFVAAWTLKAAA*

GAATTCGCCGCCACCATGGGAATGCAGGTGCAGATCCAAAGCCTGTTTCTGCTCCTCCTGTGG
GTGCCCGGCTCCAGAGGAAGGCTGGGCGTGAGAGCCACCCGGAAGAAGGCTGCCGCTAAAAC
AAGCGAGCGCTCCCAGCCCAGGAACCTGCCTGGATGCTCTTTCAGCATCTTTAATGACCTCAT
GGGGTACATTCCACTGGTGAAGTATCTGCTCCCCAGACGGGGCCCTCGCCTGAACACTCTCTG
TGGATTTGCTGATCTGATGGGGTACAGGATGTATGTCGGCGGAGTCGAACACAGAAAACTGCT
CTTCAACATCCTGGGCGGATGGGTGAAGGCTGCCGCTCTGGCCGACGGGGGATGCAGCGGCG
GAGCTTACAGGCTCATTGTCTTTCCCGATCTCGGAGTCAAATTTTGGGCAAAGCACATGTGGA
ATTTCATCGGGGTGGCCGGAGCCCTGGTCGCTTTTAAAAAGCAGCTCTTCACCTTCTCCCCAA
GACGGAACGGATACCTCGTCGCCTACCAGGCCACTGTGGCTGCAGCTCTGCTCTTCCTGCTCC
TGGCCGATGCACTCATCTTCTGCCATTCCAAGAAAAAGTATCTGGTCACCAGACATGCTGACG
TGCTGGGGTTTGGCGCCTACATGAGCAAGTGCACCTGTGGCAGCTCCGACCTGTATCACATGT
GGAACTTTATTTCTGGAATCTTTTGGGCCAAGCACATGTGGAATTTTAAGAAAGCCGCTGCAG
TCCTGGTGGGCGGCGTCCTGGCAGCCGCTTTCCTGCTCCTGGCAGACGCCAGGGTGCTGTCTG
CCTTCAGCCTCCACTCCTACATCCTCGCAGGGTATGGCGCAGGCGTGTGGATGAATCGGCTGA
TCGCCTTTGCCAATGCTGCAGCTAAATTCGTGGCAGCCTGGACACTGAAAGCAGCTGCATGAG
GATCC ∙ (SEQ ID NO:108)

AOSI.K (SEQ ID NO:109)
MGMQVQIQSLFLLLLWVPGSRGHTLWKAGILYKAKFVAAWTLKAAAFLPSDFFPSVKFLLSLGIH
LYMDDVVLGVGLSRYVARLFLLTRILTISTLPETTVVRRQAFTFSPTYKWLSLLVPFV

ATGGGAATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGGTCCAGA
GGACACACCCTGTGGAAGGCCGGAATCCTGTATAAGGCCAAGTTCGTGGCTGCCTGGACCCTG
AAGGCTGCCGCTTTCCTGCCTAGCGATTTCTTTCCTAGCGTGAAGTTCCTGCTGTCCCTGGGAA
TCCACCTGTATATGGATGACGTGGTGCTGGGAGTGGGACTGTCCAGGTACGTGGCTAGGCTGT
TCCTGCTGACCAGAATCCTGACCATCTCCACCCTGCCAGAGACCACCGTGGTGAGGAGGCAGG
CCTTCACCTTTAGCCCTACCTATAAGTGGCTGAGCCTGCTGGTGCCCTTTGTGTGA (SEQ ID NO:110)

HBV.1 (SEQ ID NO:111)
MGMQVQIQSLFLLLLWVPGSRGHTLWKAGILYKAKFVAAWTLKAAAFLPSDFFPSVFLLSLGIHL
YMDDVVLGVGLSRYVARLFLLTRILTISTLPETTVVRRQAFTFSPTYKWLSLLVPFVIPIPSSWAFTP
ARVTGGVFKVGNFTGLYLPSDFFPSVTLWKAGILYKNVSIPWTHKLVVDFSQFSRSAICSVVRRAL
MPLYACI

ATGGGAATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGGTCCAGA
GGACACACCCTGTGGAAGGCCGGAATCCTGTATAAGGCCAAGTTCGTGGCTGCCTGGACCCTG
AAGGCTGCCGCTTTCCTGCCTAGCGATTTCTTTCCTAGCGTGTTCCTGCTGTCCCTGGGAATCC
ACCTGTATATGGATGACGTGGTGCTGGGAGTGGGACTGTCCAGGTACGTGGCTAGGCTGTTCC
TGCTGACCAGAATCCTGACCATCTCCACCCTGCCAGAGACCACCGTGGTGAGGAGGCAGGCCT
TCACCTTTAGCCCTACCTATAAGTGGCTGAGCCTGCTGGTGCCCTTTGTGATCCCTATCCCTAG
CTCCTGGGCTTTCACCCCAGCCAGGGTGACCGGAGGAGTGTTTAAGGTGGGAAACTTCACCGG
CCTGTATCTGCCCAGCGATTTCTTTCCTAGCGTGACCCTGTGGAAGGCCGGGATCCTGTACAA
GAATGTGTCCATCCCTTGGACCCACAAGCTGGTGGTGGACTTTTCCCAGTTCAGCAGATCCGC
TATCTGCTCCGTGGTGAGGAGAGCTCTGATGCCACTGTATGCCTGTATCTGA (SEQ ID NO:112)

FIGURE 18G

HBV.2 (SEQ ID NO:113)
MGMQVQIQSLFLLLLWVPGSRGHTLWKAGILYKAKFVAAWTLKAAAFLPSDFFPSVNFLLSLGIH
LYMDDVVLGVGLSRYVARLFLLTRILTISTLPETTVVRRQAFTFSPTYKGAAAWLSLLVPFVNIPIP
SSWAFKTPARVTGGVFKVGNFTGLYNLPSDFFPSVKTLWKAGILYKNVSIPWTHKGAALVVDFSQ
FSRNSAICSVVRRALMPLYACI

ATGGGAATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGGTCCAGA
GGACACACCCTGTGGAAGGCCGGAATCCTGTATAAGGCCAAGTTCGTGGCTGCCTGGACCCTG
AAGGCTGCCGCTTTCCTGCCTAGCGATTTCTTTCCTAGCGTGAACTTCCTGCTGTCCCTGGGAA
TCCACCTGTATATGGATGACGTGGTGCTGGGAGTGGGACTGTCCAGGTACGTGGCTAGGCTGT
TCCTGCTGACCAGAATCCTGACCATCTCCACCCTGCCAGAGACCACCGTGGTGAGGAGGCAGG
CCTTCACCTTTAGCCCTACCTATAAGGGAGCCGCTGCCTGGCTGAGCCTGCTGGTGCCCTTTGT
GAATATCCCTATCCCTAGCTCCTGGGCTTTCAAGACCCCAGCCAGGGTGACCGGAGGAGTGTT
TAAGGTGGGAAACTTCACCGGCCTGTATAACCTGCCCAGCGATTTCTTTCCTAGCGTGAAGAC
CCTGTGGAAGGCCGGAATCCTGTACAAGAATGTGTCCATCCCTTGGACCCACAAGGGAGCCG
CTCTGGTGGTGGACTTTTCCCAGTTCAGCAGAAATTCCGCTATCTGCTCCGTGGTGAGGAGAG
CTCTGATGCCACTGTATGCCTGTATCTGA   (SEQ ID NO:114)

PfCTL.1 (SEQ ID NO:115)
MQVQIQSLFLLLLWVPGSRGILSVSSFLFVNAAAQTNFKSLLRNLPSENERGYKAAALLACAGLAY
KKAAAAKFVAAWTLKAAAKAFMKAVCVEVNAAASFLFVEALFNATPYAGEPAPFKAAAKYKLA
TSVLKAGVSENIFLKNAAAYFILVNLLIKAGLLGVVSTV

ATGGGAATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGATCCAGA
GGAATCCTGAGCGTGTCCTCTTTCCTGTTTGTCAACGCCGCTGCACAGACCAATTTCAAGAGC
CTCCTGAGGAACCTCCCCTCCGAGAACGAAAGAGGCTACAAAGCCGCTGCACTGCTCGCCTGC
GCTGGACTGGCCTATAAGAAAGCCGCTGCAGCCAAGTTCGTGGCCGCTTGGACACTGAAGGC
CGCTGCAAAAGCCTTTATGAAGGCTGTCTGTGTGGAGGTCAATGCCGCTGCATCTTTCCTGTTT
GTGGAGGCCCTCTTTAACGCTACTCCTTACGCAGGGGAACCAGCCCCCTTCAAGGCCGCTGCA
AAATATAAGCTGGCAACCAGCGTGCTGAAGGCTGGCGTGTCCGAGAATATTTTTCTGAAAAAC
GCCGCTGCATACTTCATCCTGGTGAATCTGCTCATTAAGGCCGGACTCCTGGGGGTGGTCTCT
ACAGTGTGA   (SEQ ID NO:116)

PfCTL.2 (SEQ ID NO:117)
MQVQIQSLFLLLLWVPGSRGFVEALFQEYNAAAKYLVIVFLINALACAGLAYKKFYFILVNLLKA
ALFFIIFNKNAAAKFVAAWTLKAAAKFILVNLLIFHNFQDEENIGIYKLPYGRTNLKAAAVLLGGV
GLVLNFLIFFDLFLVKAVLAGLLGVV

ATGGGAATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGATCCAGA
GGATTCGTGGAGGCCCTGTTTCAGGAATACAACGCCGCTGCAAAGTATCTCGTCATCGTGTTC
CTGATCAATGCTCTGGCATGCGCCGGCCTCGCTTACAAAAAGTTTTACTTCATTCTGGTCAACC
TGCTCAAGGCCGCTCTGTTCTTTATCATTTTCAATAAAAACGCCGCAGCTAAGTTTGTGGCCGC
ATGGACCCTGAAGGCCGCTGCAAAATTCATCCTCGTGAATCTGCTCATTTTTCACAACTTCCAA
GACGAGGAAAATATCGGAATTTATAAGCTGCCCTACGGGAGGACAAACCTGAAAGCCGCTGC
AGTCCTGCTCGGCGGAGTGGGGCTGGTGCTCAATTTTCTGATCTTCTTTGATCTGTTCCTGGTG
AAGGCCGTCCTGGCCGGCCTGCTCGGAGTCGTGTGA   (SEQ ID NO:118)

FIGURE 18H

<u>PfCTL.3</u> (SEQ ID NO:119)
MQVQIQSLFLLLLWVPGSRGVFLIFFDLFLNAAAPSDGKCNLYKAAAVTCGNGIQVRKLFHIFDGD
NEIKAHVLSHNSYEKNYYGKQENWYSLKKILSVFFLANAAAKFIKSLFHIFKAAALYISFYFIKAKF
VAAWTLKAAAKAAAYYIPHQSSLKAAAGLIMVLSFL

ATGGGAATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGATCCAGA
GGAGTGTTCCTGATCTTCTTTGACCTGTTCCTGAACGCCGCTGCACCCAGCGATGGCAAGTGC
AATCTCTACAAGGCCGCTGCAGTGACCTGTGGAAACGGGATTCAGGTCAGGAAACTCTTTCAC
ATCTTCGACGGCGATAACGAGATCAAGGCCCATGTGCTGTCCCACAATTCTTATGAAAAAAAC
TACTATGGAAAGCAAGAGAATTGGTACAGCCTGAAGAAAATTCTGTCCGTGTTCTTTCTCGCC
AACGCCGCTGCAAAGTTTATCAAGTCTCTGTTCCATATTTTCAAGGCCGCTGCACTCTACATCA
GCTTCTATTTTATTAAAGCCAAATTTGTGGCCGCTTGGACACTGAAGGCCGCTGCAAAAGCCG
CTGCATACTATATCCCTCACCAGAGCTCCCTGAAGGCCGCTGCAGGGCTGATCATGGTGCTCT
CTTTCCTGTGA (SEQ ID NO:120)

<u>PfCTL/HTL(N)</u> (SEQ ID NO:121)
MQVQIQSLFLLLLWVPGSRGSSVFNVVNSSIGLIMVLSFLGPGPGLYISFYFILVNLLIFHINGKIIKN
SEGPGPGPDSIQDSLKESRKLSGPGPGVLAGLLGVVSTVLLGGVGLVLGPGPGLPSENERGYYIPHQ
SSLGPGPGQTNFKSLLRNLGVSENIFLKGPGPGFQDEENIGIYGPGPGKYLVIVFLIFFDLFLVGPGP
GKFIKSLFHIFDGDNEIGPGPGKSKYKLATSVLAGLLGPGPGLPYGKTNLGPGPGRHNWVNHAVPL
AMKLIGPGPGMRKLAILSVSSFLFVEALFQEYGPGPGVTCGNGIQVRGPGPGMNYYGKQENWYSL
KKGPGPGPSDGKCNLYADSAWENVKNVIGPFMKAVCVEVGPGPGKILSVFFLALFFIIFNKGPGPG
HVLSHNSYEKGPGPGKYKIAGGIAGGLALLACAGLAYKFVVPGAATPYAGEPAPF

ATGGGAATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGATCCAGA
GGAAGTAGTGTGTTCAATGTTGTGAACTCATCAATTGGTCTGATCATGGTGCTGAGCTTTCTCG
GGCCAGGGCCAGGATTATATATTTCTTTCTACTTCATCCTTGTCAACCTGTTAATATTCCACAT
TAACGGCAAAATAATAAAGAACAGTGAAGGCCCTGGGCCTGGGCTGACTCGATCCAGGATT
CTCTAAAAGAATCGAGGAAGCTCTCCGGACCAGGCCCTGGTGTACTCGCCGGGTTGCTGGGA
GTAGTTAGCACAGTGCTGTTAGGAGGCGTCGGCCTCGTCTTAGGACCTGGACCAGGTCTGCCG
TCCGAAAACGAAAGAGGATACTACATACCTCACCAGAGCAGCCTCGGCCCAGGCCCCGGACA
AACCAATTTCAAATCCCTCTTGCGAAATCTAGGAGTGAGCGAGAACATATTTCTTAAAGGACC
CGGTCCCGGCTTTCAGGACGAGGAGAATATAGGTATTTACGGTCCAGGACCTGGAAAATACCT
AGTGATCGTATTCCTAATTTTTTTTGACCTATTTCTGGTGGGCCCAGGTCCCGGAAAGTTCATT
AAATCACTCTTCCACATTTTTGACGGAGATAACGAGATAGGACCCGGTCCCGGGAAATCAAA
GTACAAACTAGCCACTTCAGTGCTGGCCGGCCTTCTAGGGCCGGGCCCAGGGCTCCCCTATGG
AAAGACAAATCTTGGCCCCGGTCCAGGACGGCACAACTGGGTGAATCATGCGGTTCCATTGG
CCATGAAACTAATCGGGCCCGGTCCAGGCATGCGCAAACTTGCAATTCTAAGCGTAAGTTCAT
TTCTGTTCGTAGAGGCACTGTTTCAAGAATATGGCCCAGGACCTGGCGTCACATGTGGGAATG
GGATCCAGGTGAGAGGACCGGGACCTGGTATGAACTATTACGGTAAACAGGAAAATTGGTAC
TCCCTGAAAAAGGGTCCAGGCCCCGGCCCCTCAGATGGTAAGTGCAACCTGTATGCTGACTCA
GCATGGGAGAACGTAAAAAATGTAATAGGCCCATTCATGAAGGCAGTTTGTGTCGAAGTCGG
ACCAGGCCCAGGAAAAATACTTTCTGTCTTCTTCCTAGCTCTCTTCTTCATCATCTTCAACAAG
GGACCAGGGCCAGGTCACGTGTTATCCCATAACTCTTATGAAAAAGGGCCAGGACCTGGGAA
ATACAAAATCGCAGGAGGGATCGCCGGCGGGCTAGCGCTCCTTGCCTGCGCAGGCTTGGCTTA
CAAATTCGTTGTACCAGGAGCTGCAACACCCTATGCAGGAGAACCTGCCCCATTTTGAAGATC
TGC (SEQ ID NO:122)

FIGURE 18I

Pf33 (SEQ ID NO:123)
MGMQVQIQSLFLLLLWVPGSRGFMKAVCVEVNVTCGNGIQVRKGLIMVLSFLNAALFHIFDGDN
EIKAALLACAGLAYKKSFLFVEALFNAAPSDGKCNLYKAAQTNFKSLLRNLPSENERGYKAAGVS
ENIFLKNAAAYFILVNLLIKAAAILSVSSFLFVNTPYAGEPAPFKAAAKYKLATSVLKAAVFLIFFDL
FLNYYIPHQSSLKAAGLLGNVSTVGAVLLGGVGLVLNLACAGLAYKKAKFIKSLFHIFKAAFYFIL
VNLLKAFLIFFDLFLVKALFFIIFNKNYYGKQENWYSLKFVEALFQEYNAAAKFVAAWTLKAAAK
ILSVFFLANAVLAGLLGNVNFQDEENIGIYKAAALYISFYFIKAFILVNLLIFHNAALPYGRTNLKAA
HVLSHNSYEKNAAAKYLVIVFLI

GCCGCCACCATGGGAATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCC
GGATCCAGAGGATTTATGAAAGCTGTCTGTGTAGAGGTGAATGTAACATGCGGTAACGGAAT
TCAGGTGAGAAAGGGACTCATCATGGTACTCAGCTTTCTGAACGCAGCCCTGTTCCACATCTT
TGACGGAGACAATGAAATCAAAGCCGCATTGCTCGCCTGTGCCGGACTAGCCTATAAAAAGA
GTTTCCTTTTCGTTGAAGCACTATTTAACGCAGCACCCAGTGACGGTAAATGCAACCTATATA
AAGCAGCTCAGACTAATTTCAAAAGCCTGTTAAGAAATCTGCCCTCAGAGAATGAAAGGGGT
TACAAAGCCGCCGGCGTGTCCGAGAATATTTTCCTGAAGAACGCCGCTGCTTATTTTATACTC
GTGAATCTACTCATAAAGGCAGCCGCAATCCTTTCAGTGTCCAGCTTTCTGTTTGTTAACACAC
CATATGCGGGCGAGCCGGCTCCTTTCAAGGCTGCAGCAAAATACAAGCTTGCCACATCAGTAT
TGAAAGCAGCTGTGTTTTTGATATTCTTTGATCTTTTTTTAAACTACTACATACCTCATCAGTCT
AGTCTTAAAGCAGCCGGGCTACTGGGGAACGTCTCTACTGTGGGGGCCGTCTTACTTGGAGGA
GTTGGCCTCGTGTTGAACCTCGCGTGCGCAGGTCTGGCCTACAAAAAAGCGAAATTCATCAAG
TCTCTGTTCCACATTTTTAAAGCCGCATTCTATTTCATACTAGTGAACCTTCTCAAAGCTTTCCT
GATCTTCTTCGATCTATTCCTCGTAAAAGCGCTATTCTTCATTATCTTTAACAAAAATTATTAC
GGCAAGCAAGAAAATTGGTACTCACTCAAGTTTGTAGAAGCTCTGTTCCAGGAATACAACGCC
GCTGCTAAATTCGTTGCAGCTTGGACCCTGAAAGCAGCTGCAAAGATCCTATCGGTCTTCTTTC
TCGCTAATGCCGTATTAGCAGGACTTCTAGGCAACGTGAACTTTCAAGACGAAGAGAATATAG
GCATCTACAAAGCCGCAGCACTGTACATTTCATTCTACTTCATCAAGGCCTTCATACTGGTCAA
CCTTCTGATATTTCATAATGCAGCACTGCCATATGGGAGAACCAACTTGAAAGCGGCCCACGT
GTTGAGCCACAACTCCTACGAGAAGAACGCCGCCGCGAAATATCTCGTCATTGTCTTCCTGAT
TTGA (SEQ ID NO:124)

TB.1 (SEQ ID NO:125)
MQVQIQSLFLLLLWVPGSRGRMSRVTTFTVKALVLLMLPVVNLMIGTAAAVVKALVLLMLPVGA
GLMTAVYLVGAAAMALLRLPVKRMFAANLGVNSLYFGGICVGRLPLVLPAVNAAAAKFVAAWT
LKAAAKAAARLMIGTAAAGFVVALIPLVNAMTYAAPLFVGAAAAMALLRLPLV

ATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGATCCAGAGGAAGG
ATGAGCAGAGTGACCACATTCACTGTCAAGGCCCTGGTGCTCCTGATGCTCCCCGTCGTGAAC
CTGATGATCGGCACCGCTGCAGCCGTCGTGAAAGCTCTCGTCCTGCTCATGCTCCCTGTGGGA
GCAGGGCTGATGACAGCCGTGTACCTGGTCGGCGCTGCAGCCATGGCCCTCCTGCGGCTGCCA
GTGAAGCGCATGTTTGCTGCAAATCTGGGAGTCAACTCCCTCTATTTCGGGGGCATTTGCGTG
GGAAGGCTGCCCCTCGTGCTGCCTGCTGTGAATGCAGCCGCTGCCAAATTTGTCGCCGCTTGG
ACTCTGAAGGCAGCCGCTAAGGCCGCTGCAAGACTGATGATCGGGACCGCCGCTGCCGGCTT
CGTGGTCGCCCTGATTCCCCTGGTGAACGCCATGACATACGCAGCTCCTCTGTTTGTGGGAGC
CGCTGCAGCCATGGCTCTCCTGCGGCTGCCACTGGTGTGA (SEQ ID NO:126)

FIGURE 18J

BCL A2 #90 (SEQ ID NO:127)
MQVQIQSLFLLLLWVPGSRGIMIGHLVGVNRLLQETELVNAKVAEIVHFLNAKVFGSLAFVNAYL
SGANLNVGAAYLQLVFGIEVNAAAKFVAAWTLKAAAKAAAVVLGVVFGINSMPPPGTRVNAAA
ATVGIMIGVNAKLCPVQLWV

ATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGGTCCAGAGGAATT
ATGATCGGCCATCTGGTGGGCGTCAACAGACTGCTGCAGGAAACCGAGCTGGTGAATGCCAA
GGTGGCCGAAATTGTGCACTTTCTCAACGCAAAGGTGTTTGGTTCCCTGGCTTTTGTCAATGCC
TATCTGAGCGGCGCTAACCTCAACGTCGGAGCCGCCTACCTCCAGCTGGTCTTCGGCATCGAG
GTCAACGCTGCTGCAAAATTCGTGGCAGCTTGGACCCTCAAGGCTGCAGCAAAGGCTGCCGCC
GTCGTGCTCGGAGTGGTGTTCGGGATCAACTCTATGCCACCTCCCGGGACTAGGGTCAATGCT
GCCGCCGCAACAGTGGGAATCATGATTGGGGTGAATGCCAAACTGTGCCCAGTGCAACTGTG
GGTGTGA (SEQ ID NO:128)

BCL A2 #88 (SEQ ID NO:129)
MQVQIQSLFLLLLWVPGSRGVVLGVVFGINAAAAKFVAAWTLKAAAKVAEIVHFLNAYLSGANL
NVGAAYLQLVFGIEVNIMIGHLVGVNRLLQETELVNAKVFGSLAFVNAKLCPVQLWVNAAAATV
GIMIGVNSMPPPGTRV

ATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGGTCCAGAGGAGTC
GTGCTGGGAGTCGTCTTCGGCATTAATGCCGCCGCTGCAAAGTTCGTGGCTGCCTGGACCCTG
AAGGCCGCAGCTAAAGTGGCAGAGATCGTGCACTTTCTGAACGCCTACCTGAGCGGAGCAAA
TCTGAACGTCGGCGCTGCCTATCTGCAGCTCGTGTTTGGAATTGAAGTGAACATCATGATTGG
ACATCTGGTGGGCGTGAACAGGCTGCTCCAGGAAACTGAGCTGGTCAACGCTAAAGTGTTCG
GGTCTCTCGCCTTTGTGAACGCTAAGCTCTGCCCCGTCCAACTCTGGGTCAATGCCGCAGCCG
CTACAGTGGGGATCATGATCGGCGTGAACTCCATGCCTCCACCAGGGACCAGAGTGTGA
(SEQ ID NO:130)

BCL A2 #63 (SEQ ID NO:131)
MQVQIQSLFLLLLWVPGSRGKLCPVQLWVNAAAATVGIMIGVNIMIGHLVGVNRLLQETELVNA
KVAEIVHFLNAKVFGSLAFVNAYLSGANLNVGAAYLQLVFGIEVNAAAKFVAAWTLKAAAKAA
AVVLGVVFGINSMPPPGTRV

ATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGGTCCAGAGGAAAG
CTCTGCCCCGTGCAACTGTGGGTCAACGCCGCCGCCGCAACCGTCGGCATTATGATCGGGGTG
AACATCATGATCGGACACCTGGTCGGCGTGAACAGGCTGCTGCAGGAGACAGAACTGGTCAA
TGCCAAGGTGGCTGAAATTGTCCATTTCCTGAATGCCAAAGTGTTCGGCTCTCTCGCTTTCGTG
AACGCTTATCTGAGCGGAGCTAACCTCAACGTGGGGGCCGCATACCTCCAGCTCGTCTTTGGG
ATTGAGGTGAATGCCGCAGCTAAATTTGTCGCTGCCTGGACCCTGAAGGCAGCAGCCAAGGCT
GCCGCAGTGGTGCTGGGAGTGGTGTTTGGAATCAATTCCATGCCTCCACCAGGCACTAGAGTG
TGAGGATCC (SEQ ID NO:132)

FIGURE 18K

Prostate 1 (SEQ ID NO:133)
LTFFWLDRSVKAAAVLVHPQWVLTVKAAALLQERGVAYIKAALLLSIALSVNPLVCNGVLQGVK
AAIMYSAHDTTVKAAAFLTPKKLQCVNAMMNDQLMFLNAGLPSIPVHPVKAAALGTTCYVGAAI
LLWQPIPVNFLRPRSLQCVKAFLTLSVTWIGVNALLYSLVHNLGAATLMSAMTNL

ATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGGTCCAGAGGATTG
ACATTTTTTTGGCTGGATAGATCGGTTAAGGCTGCAGCCGTGCTTGTTCATCCCCAGTGGGTCT
TGACCGTAAAGGCTGCCGCGCTGCTACAAGAAAGAGGGGTCGCATACATCAAAGCTGCTCTC
CTCTTGAGTATTGCGCTAAGTGTAAACCCGCTAGTTTGTAATGGGGTGTTACAAGGTGTGAAA
GCGGCGATTATGTACAGTGCCCACGACACTACCGTAAAAGCAGCCGCTTTCCTGACCCCAAAA
AAACTCCAATGCGTGAACGCAATGATGAATGATCAGCTGATGTTTTTAAACGCTGGCTTACCT
TCTATACCGGTTCATCCAGTCAAGGCCGCGGCATTGGGTACGACGTGTTATGTTGGAGCAGCG
ATACTTCTTTGGCAGCCCATACCAGTAAATTTTTTAAGACCTAGATCCTTACAATGCGTCAAAG
CATTCCTTACACTCTCAGTAACTTGGATCGGAGTCAATGCTCTGCTATATAGCCTCGTACACAA
CTTGGGCGCGGCCACACTTATGAGTGCAATGACGAATTTAGCTAAGTTCGTGGCGGCCTGGAC
TCTAAAGGCCGCAGCA (SEQ ID NO:134)

HIV-1043 (SEQ ID NO:135)
MEKVYLAWVPAHKGIGGGPGPGQKQITKIQNFRVYYRGPGPGWEFVNTPPLVKLWYQGPGPGYR
KILRQRKIDRLIDGPGPGQHLLQLTVWGIKQLQGPGPGGEIYKRWIILGLNKIVRMYGPGPGQGQM
VHQAISPRTLNGPGPGIKQFINMWQEVGKAMYGPGPGWAGIKQEFGIPYNPQGPGPGKTAVQMA
VFIHNFKRGPGPGSPAIFQSSMTKILEPGPGPGEVNIVTDSQYALGIIGPGPGHSNWRAMASDFNLPP
GPGPGAETFYVDGAANRETKGPGPGGAVVIQDNSDIKVVPGPGPGFRKYTAFTIPSINNE

ATGGAGAAGGTGTACCTGGCCTGGGTTCCAGCCCACAAAGGCATCGGGGGAGGGCCCGGACC
TGGGCAGAAACAGATCACCAAGATCCAGAACTTCCGGGTATACTACCGGGGACCTGGTCCAG
GTTGGGAGTTTGTGAACACACCACCCTTAGTAAAGCTCTGGTACCAGGGCCCCGGTCCCGGAT
ACCGTAAAATCCTGAGGCAAAGAAAGATAGATCGCCTCATTGATGGCCCGGGCCCAGGCCAG
CACCTTCTGCAGCTTACAGTGTGGGGAATTAAACAGCTGCAGGGGCCGGGCCCCGGGGGGGA
AATTTATAAAAGGTGGATCATTCTGGGTCTGAACAAGATCGTCCGCATGTATGGCCCTGGACC
CGGACAGGGGCAGATGGTCCACCAAGCAATCAGCCCTCGAACCTTGAATGGACCGGGCCCAG
GAATCAAGCAATTCATTAACATGTGGCAAGAAGTTGGTAAGGCTATGTACGGTCCCGGCCCTG
GATGGGCAGGGATAAAACAGGAGTTTGGAATCCCTTACAATCCCCAGGGTCCTGGGCCAGGT
AAAACGGCAGTGCAGATGGCCGTGTTCATTCATAATTTTAAGCGGGGCCCTGGACCTGGCAGC
CCAGCTATATTTCAAAGTTCGATGACCAAAATCTTGGAGCCCGGCCCAGGGCCGGGCGAAGT
GAACATTGTCACAGATTCTCAGTATGCCCTCGGCATCATAGGGCCCGGACCAGGGCATTCCAA
TTGGCGCGCCATGGCGTCTGACTTTAATCTACCTCCTGGGCCAGGCCCTGGCGCGGAAACTTT
CTATGTGGACGGCGCTGCAAACAGGGAGACTAAGGGACCCGGACCCGGCGGCGCTGTAGTCA
TTCAGGACAACTCAGACATCAAGGTGGTTCCCGGTCCAGGCCCCGGGTTCAGAAAGTATACCG
CCTTCACTATTCCGTCCATCAACAATGAGTGA (SEQ ID NO:136)

FIGURE 18L

<u>HIV-1043 PADRE</u> (SEQ ID NO:137)
MEKVYLAWVPAHKGIGGGPGPGQKQITKIQNFRVYYRGPGPGWEFVNTPPLVKLWYQGPGPGYR
KILRQRKIDRLIDGPGPGQHLLQLTVWGIKQLQGPGPGGEIYKRWIILGLNKIVRMYGPGPGQGQM
VHQAISPRTLNGPGPGIKQFINMWQEVGKAMYGPGPGWAGIKQEFGIPYNPQGPGPGKTAVQMA
VFIHNFKRGPGPGSPAIFQSSMTKILEPGPGPGEVNIVTDSQYALGIIGPGPGHSNWRAMASDFNLPP
GPGPGAETFYVDGAANRETKGPGPGGAVVIQDNSDIKVVPGPGPGFRKYTAFTIPSINNEGPGPGA
KFVAAWTLKAAA

ATGGAGAAGGTGTACCTGGCCTGGGTTCCAGCCCACAAAGGCATCGGGGGAGGGCCCGGACC
TGGGCAGAAACAGATCACCAAGATCCAGAACTTCCGGGTATACTACCGGGGACCTGGTCCAG
GTTGGGAGTTTGTGAACACACCACCCTTAGTAAAGCTCTGGTACCAGGGCCCCGGTCCCGGAT
ACCGTAAAATCCTGAGGCAAAGAAAGATAGATCGCCTCATTGATGGCCCGGGCCCAGGCCAG
CACCTTCTGCAGCTTACAGTGTGGGGAATTAAACAGCTGCAGGGGCCGGGCCCCGGGGGGGA
AATTTATAAAAGGTGGATCATTCTGGGTCTGAACAAGATCGTCCGCATGTATGGCCCTGGACC
CGGACAGGGGCAGATGGTCCACCAAGCAATCAGCCCTCGAACCTTGAATGGACCGGGCCCAG
GAATCAAGCAATTCATTAACATGTGGCAAGAAGTTGGTAAGGCTATGTACGGTCCCGGCCCTG
GATGGGCAGGGATAAAACAGGAGTTTGGAATCCCTTACAATCCCCAGGGTCCTGGGCCAGGT
AAAACGGCAGTGCAGATGGCCGTGTTCATTCATAATTTTAAGCGGGGCCCTGGACCTGGCAGC
CCAGCTATATTTCAAAGTTCGATGACCAAAATCTTGGAGCCCGGCCCAGGGCCGGGCGAAGT
GAACATTGTCACAGATTCTCAGTATGCCCTCGGCATCATAGGGCCCGGACCAGGGCATTCCAA
TTGGCGCGCCATGGCGTCTGACTTTAATCTACCTCCTGGGCCAGGCCCTGGCGCGGAAACTTT
CTATGTGGACGGCGCTGCAAACAGGGAGACTAAGGGACCCGGACCCGGCGGCGCTGTAGTCA
TTCAGGACAACTCAGACATCAAGGTGGTTCCCGGTCCAGGCCCCGGGTTCAGAAAGTATACCG
CCTTCACTATTCCGTCCATCAACAATGAGGGCCCCGGCCCAGGTGCCAAGTTCGTGGCTGCCT
GGACCCTGAAGGCTGCCGCTTGA (SEQ ID NO:138)

<u>HIV 75mer</u> (SEQ ID NO:139)
EKVYLAWVPAHKGIGGPGPGQGQMVHQAISPRTLNGPGPGSPAIFQSSMTKILEPGPGPGFRKYTA
FTIPSINNE

GAGAAGGTGTACCTGGCCTGGGTGCCTGCCCACAAGGGAATCGGAGGACCTGGCCCTGGACA
GGGACAGATGGTGCACCAGGCCATCAGCCCTAGGACCCTGAACGGACCTGGACCTGGAAGCC
CTGCCATCTTCCAGAGCAGCATGACCAAGATCCTGGAGCCCGGACCTGGACCTGGATTCAGGA
AGTACACCGCCTTCACCATCCCCAGCATCAACAACGAGTGA (SEQ ID NO:140)

FIGURE 18M

PfHTL (SEQ ID NO:141)
MQVQIQSLFLLLLWVPGSRGRHNWVNHAVPLAMKLIGPGPGKCNLYADSAWENVKNGPGPGKS
KYKLATSVLAGLLGPGPGQTNFKSLLRNLGVSEGPGPGSSVFNVVNSSIGLIMGPGPGVKNVIGPF
MKAVCVEGPGPGMNYYGKQENWYSLKKGPGPGGLAYKFVVPGAATPYGPGPGPDSIQDSLKESR
KLNGPGPGLLIFHINGKIIKNSEGPGPGAGLLGNVSTVLLGGVGPGPGKYKIAGGIAGGLALLGPGP
GMRKLAILSVSSFLFV

ATGGGAATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGATCCAGA
GGAAGGCACAACTGGGTGAATCATGCTGTGCCCCTGGCTATGAAGCTGATCGGCCCTGGACC
AGGGAAATGCAACCTCTACGCAGACAGCGCCTGGGAGAACGTCAAGAATGGCCCCGGACCTG
GGAAATCCAAGTATAAGCTCGCTACCTCTGTGCTGGCAGGCCTGCTCGGACCAGGCCCCGGAC
AGACAAATTTCAAAAGCCTGCTCAGAAACCTGGGAGTGTCCGAGGGGCCTGGCCCAGGATCT
AGCGTCTTTAATGTGGTCAACTCCTCTATTGGGCTCATCATGGGACCCGGACCTGGGGTGAAA
AATGTCATTGGCCCATTCATGAAGGCCGTGTGTGTCGAAGGACCCGGGCCTGGCATGAACTAC
TATGGAAAGCAAGAAAATTGGTACAGCCTGAAGAAAGGCCCTGGGCCAGGCGGACTGGCTTA
CAAGTTTGTGGTCCCAGGGGCAGCCACTCCCTATGGGCCTGGGCCAGGCCCCGATTCCATCCA
GGACTCTCTCAAAGAGAGCCGGAAACTGAACGGACCCGGGCCTGGACTGCTCATTTTCCACAT
CAATGGCAAAATTATCAAGAACAGCGAGGGACCTGGGCCAGGCGCCGGACTGCTGGGGAACG
TGTCCACCGTCCTGCTCGGCGGAGTGGGGCCCGGCCCTGGGAAGTACAAGATCGCTGGAGGG
ATCGCAGGCGGACTGGCCCTCCTGGGCCCAGGACCAGGGATGCGCAAACTGGCTATTCTCTCT
GTCTCCAGCTTTCTGTTTGTGTGA (SEQ ID NO:142)

FIGURE 18N

Protein	Sequence(SEQ ID NOS:143-340)	Restriction
HIV gag 386	VLAEAMSQV	HLA-A2
HIV gag 271	MTNNPPIPV	HLA-A2
HIV pol 774	MASDFNLPPV	HLA-A2
HIV pol 448	KLVGKLNWA	HLA-A2
HIV pol 163	LVGPTPVNI	HLA-A2
HIV pol 498	ILKEPVHGV	HLA-A2
HIV pol 879	KAACWWAGI	HLA-A2
HIV pol 132	KMIGGIGGFI	HLA-A2
HIV pol 772	RAMASDFNL	HLA-A2
HIV pol 183	TLNFPISPI	HLA-A2
HIV env 134	KLTPLCVTL	HLA-A2
HIV env 651	LLQLTVWGI	HLA-A2
HIV env 163	SLLNATDIAV	HLA-A2
HIV nef 221	LTFGWCFKL	HLA-A2
HIV vpr 59	AIIRILQQL	HLA-A2
HIV vpr 62	RILQQLLFI	HLA-A2
HIV pol 929	QMAVFIHNFK	HLA-A3
HIV pol 722	KVYLAWVPAHK	HLA-A3
HIV pol 971	KIQNFRVYYR	HLA-A3
HIV pol 347	AIFQSSMTK	HLA-A3
HIV pol 98	VTIKIGGQLK	HLA-A3
HIV env 61	TTLFCASDAK	HLA-A3
HIV env 47	VTVYYGVPVWK	HLA-A3
HIV nef 100	QVPLRPMTYK	HLA-A3
HIV vif 7	VMIVWQVDR	HLA-A3
HIV gag 162	QMVHQAISPR	HLA-A3
HIV gag 545	YPLASLRSLF	HLA-B7
HIV gag 237	HPVHAGPIA	HLA-B7
HIV pol 186	FPISPIETV	HLA-B7
HIV pol 893	IPYNPQSQGVV	HLA-B7
HIV env 259	IPIHYCAPA	HLA-B7
HIV env 250	CPKVSFEPI	HLA-B7
HIV nef 94	FPVRPQVPL	HLA-B7
HIV rev 75	VPLQLPPL	HLA-B7
HIV pol 684	EVNIVTDSQY	HLA-A1
HIV gag 317	FRDYVDRFY	HLA-A1
HIV pol 368	VIYQYMDDLY	HLA-A1
HIV pol 295	VTVLDVGDAY	HLA-A1
HIV pol 533	IYQEPFKNL	HLA-A24
HIV pol 244	PYNTPVFAI	HLA-A24
HIV pol 530	TYQIYQEPF	HLA-A24
HIV pol 597	YWQATWIPEW	HLA-A24
HIV env 681	IWGCSGKLI	HLA-A24
HIV env 671	RYLKDQQLL	HLA-A24

FIGURE 19A

Protein	Sequence	Restriction
HIV env 55	VWKEATTTLF	HLA-A24
HIV vpr 46	IYETYGDTW	HLA-A24
HIV vpr 14	PYNEWTLEL	HLA-A24
HIV gag 298	KRWIILGLNKIVRMY	HLA-DR
HIV pol 596	WEFVNTPPLVKLWYQ	HLA-DR
HIV pol 956	QKQITKIQNFRVYYR	HLA-DR
HIV pol 712	KVYLAWVPAHKGIGG	HLA-DR
HIV gag 294	GEIYKRWIILGLNKI	HLA-DR
HIV pol 711	EKVYLAWVPAHKGIG	HLA-DR
HIV env 729	QHLLQLTVWGIKQLQ	HLA-DR
HIV gag 171	QGQMVHQAISPRTLN	HLA-DR
HIV pol 335	SPAIFQSSMTKILEP	HLA-DR
HIV env 566	IKQFINMWQEVGKAMY	HLA-DR
HIV pol 303	FRKYTAFTIPSINNE	HLA-DR
HIV pol 758	HSNWRAMASDFNLPP	HLA-DR
HIV pol 915	KTAVQMAVFIHNFKR	HLA-DR
HIV vpu 31	YRKILRQRKIDRLID	HLA-DR3
HIV pol 874	WAGIKQEFGIPYNPQ	HLA-DR3
HIV pol 674	EVNIVTDSQYALGII	HLA-DR3
HIV pol 619	AETFYVDGAANRETK	HLA-DR3
HIV pol 989	GAVVIQDNSDIKVVP	HLA-DR3
HCV NS4 1812	LLFNILGGWV	HLA-A2
HCV NS1/E2 728	FLLLADARV	HLA-A2
HCV NS4 1590	YLVAYQATV	HLA-A2
HCV NS5 2611	RLIVFPDLGV	HLA-A2
HCV CORE 132	DLMGYIPLV	HLA-A2
HCV NS4 1920	WMNRLIAFA	HLA-A2
HCV NS4 1666	VLVGGVLAA	HLA-A2
HCV NS4 1769	HMWNFISGI	HLA-A2
HCV NS4 1851	ILAGYGAGV	HLA-A2
HCV CORE 35	YLLPRRGPRL	HLA-A2
HCV NS1/E2 726	LLFLLLADA	HLA-A2
HCV LORF 1131	YLVTRHADV	HLA-A2
HCV CORE 51	KTSERSQPR	HLA-A3
HCV CORE 43	RLGVRATRK	HLA-A3
HCV ENV1 290	QLFTFSPRR	HLA-A3
HCV NS1/E2 632	RMYVGGVEHR	HLA-A3
HCV NS3 1396	LIFCHSKKK	HLA-A3
HCV NS4 1863	GVAGALVAFK	HLA-A3
HCV NS4 1864	VAGALVAFK	HLA-A3
HCV NS3 1262	LGFGAYMSK	HLA-A3
HCV Core 169	LPGCSFSIF	HLA-B7
HCV NS5 2922	LSAFSLHSY	HLA-A1
HCV NS3 1128	CTCGSSDLY	HLA-A1
HCV NS5 2180	LTDPSHITA	HLA-A1

FIGURE 19B

Protein	Sequence	Restriction
HCV Core 126	LTCGFADLMGY	HLA-A1
HCV NS3 1305	LADGGCSGGAY	HLA-A1
HCV NS4 1765	FWAKHMWNF	HLA-A24
HCV NS5 2875	RMILMTHFF	HLA-A24
HCV NS5 2639	VMGSSYGF	HLA-A24
HCV NS4 1765	FWAKHMWNFI	HLA-A24
P. falciparum SSP2-230	FMKAVCVEV	HLA-A2
P. falciparum EXP1-83	GLLGVVSTV	HLA-A2
P. falciparum CSP-7	ILSVSSFLFV	HLA-A2
P. falciparum LSA1-94	QTNFKSLLR	HLA-A3
P. falciparum LSA1-105	GVSENIFLK	HLA-A3
P. falciparum SSP2-522	LLACAGLAYK	HLA-A3
P. falciparum SSP2-539	TPYAGEPAPF	HLA-B7
P. falciparum LSA1-1663	LPSENERGY	HLA-A1
P. falciparum EXP1-73	KYKLATSVL	HLA-A24
P. falciparum CSP-12	SFLFVEALF	HLA-A24
P. falciparum LSA1-10	YFILVNLLI	HLA-A24
P. falciparum SSP2-14	FLIFFDLFLV	HLA-A2
P. falciparum EXP1-80	VLAGLLGVV	HLA-A2
P. falciparum EXP1-91	VLLGGVGLVL	HLA-A2
P. falciparum SSP2-523	LACAGLAYK	HLA-A3
P. falciparum EXP1-10	ALFFIIFNK	HLA-A3
P. falciparum LSA1-11	FILVNLLIFH	HLA-A3
P. falciparum SSP2-126	LPYGRTNL	HLA-B7
P. falciparum CSP-15	FVEALFQEY	HLA-A1
P. falciparum LSA1-1794	FQDEENIGIY	HLA-A1
P. falciparum LSA1-9	FYFILVNLL	HLA-A24
P. falciparum SSP2-8	KYLVIVFLI	HLA-A24
P. falciparum CSP-394	GLIMVLSFL	HLA-A2
P. falciparum EXP1-2	KILSVFFLA	HLA-A2
P. falciparum CSP-344	VTCGNGIQVR	HLA-A3
P. falciparum LSA1-59	HVLSHNSYEK	HLA-A3
P. falciparum SSP2-207	PSDGKCNLY	HLA-A1
P. falciparum LSA1-1671	YYIPHQSSL	HLA-A24
P. falciparum LSA1-1876	KFIKSLFHIF	HLA-A24
P. falciparum SSP2-13	VFLIFFDLFL	HLA-A24
P. falciparum LSA1-1881	LFHIFDGDNEI	HLA-A24
P. falciparum CSP-55	YYGKQENWYSL	HLA-A24
P. falciparum LSA1-5	LYISFYFI	HLA-A24
P. falciparum CSP-2	MRKLAILSVSSFLFV	HLA-DR
P. falciparum CSP-53	MNYYGKQENWYSLKK	HLA-DR
P. falciparum CSP-375	SSVFNVVNSSIGLIM	HLA-DR
P. falciparum SSP2-61	RHNWVNHAVPLAMKLI	HLA-DR
P. falciparum SSP2-165	PDSIQDSLKESRKLN	HLA-DR3
P. falciparum SSP2-211	KCNLYADSAWENVKN	HLA-DR3

FIGURE 19C

Protein	Sequence	Restriction
P. falciparum SSP2-223	VKNVIGPFMKAVCVE	HLA-DR
P. falciparum SSP2-509	KYKIAGGIAGGLALL	HLA-DR
P. falciparum SSP2-527	GLAYKFVVPGAATPY	HLA-DR
P. falciparum EXP1-71	KSKYKLATSVLAGLL	HLA-DR
P. falciparum EXP1-82	AGLLGNVSTVLLGGV	HLA-DR
P. falciparum LSA1-16	LLIFHINGKIIKNSE	HLA-DR
P. falciparum LSA1-94	QTNFKSLLRNLGVSE	HLA-DR
HBV core 18	FLPSDFFPSV	HLA-A2
HBV env 183	FLLTRILTI	HLA-A2
HBV env 335	WLSLLVPFV	HLA-A2
HBV pol 455	GLSRYVARL	HLA-A2
HBV pol 538	YMDDVVLGV	HLA-A2/A1
HBV pol 773	ILRGTSFVYV	HLA-A2
HBV pol 562	FLLSLGIHL	HLA-A2
HBV pol 642	ALMPLYACI	HLA-A2
HBV env 338	GLSPTVWLSV	HLA-A2
HBV core 141	STLPETTVVRR	HLA-A3
HBV pol 149	HTLWKAGILYK	HLA-A3/A1
HBV pol 150	TLWKAGILYK	HLA-A3
HBV pol 388	LVVDFSQFSR	HLA-A3
HBV pol 47	NVSIPWTHK	HLA-A3
HBV pol 531	SAICSVVRR	HLA-A3
HBV pol 629	KVGNFTGLY	HLA-A3/A1
HBV pol 665	QAFTFSPTYK	HLA-A3
HBV core 19	LPSDFFPSV	HLA-B7
HBV env 313	IPIPSSWAF	HLA-B7
HBV pol 354	TPARVTGGVF	HLA-B7
TB	RMSRVTTFTV	HLA-A2
TB	ALVLLMLPVV	HLA-A2
TB	LMIGTAAAVV	HLA-A2
TB	ALVLLMLPV	HLA-A2
TB	GLMTAVYLV	HLA-A2
TB	MALLRLPV	HLA-A2
TB	RMFAANLGV	HLA-A2
TB	SLYFGGICV	HLA-A2
TB	RLPLVLPAV	HLA-A2
TB	RLMIGTAAA	HLA-A2
TB	FVVALIPLV	HLA-A2
TB	MTYAAPLFV	HLA-A2
TB	AMALLRLPLV	HLA-A2
p53 139	KLCPVQLWV	HLA-A2
CEA 687	ATVGIMIGV	HLA-A2
CEA 691	IMIGHLVGV	HLA-A2
Her2/neu 689	RLLQETELV	HLA-A2
MAGE3 112	KVAEIVHFL	HLA-A2

FIGURE 19D

Protein	Sequence	Restriction
Her2/neu 369	KVFGSLAFV	HLA-A2
CEA 605	YLSGANLNV	HLA-A2
MAGE2 157	YLQLVFGIEV	HLA-A2
Her2/neu 665	VVLGVVFGI	HLA-A2
p53 149	SMPPPGTRV	HLA-A2
PAP.21.T2	LTFFWLDRSV	HLA-A2
PAP.112	TLMSAMTNL	HLA-A2
PAP.284	IMYSAHDTTV	HLA-A2
PSM.288.V10	GLPSIPVHPV	HLA-A2
PSM.441	LLQERGVAYI	HLA-A2
PSM.469L2	LLYSLVHNL	HLA-A2
PSM.663	MMNDQLMFL	HLA-A2
PSA.3.V11	FLTLSVTWIGV	HLA-A2
PSA.143.V8	ALGTTCYV	HLA-A2
PSA.161	FLTPKKLQCV	HLA-A2
HuK2.4.L2	LLLSIALSV	HLA-A2
HuK2.53.V11	VLVHPQWVLTV	HLA-A2
HuK2.165	FLRPRSLQCV	HLA-A2
HuK2.216.V11	PLVCNGVLQGV	HLA-A2

FIGURE 19E